AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of the Claims

1. (Currently Amended) A method for detecting ~~members of a set of polymorphisms that occur~~ a genetic marker ~~at identified loci~~ in ~~samples of~~ a patient sample nucleic acid, comprising the steps of:

providing the patient sample nucleic acid containing multiple loci at a site;

providing at least one blocker that is complementary to at least one loci of the multiple loci contained in the patient sample nucleic acid; ~~one or more blockers, the blockers being selected for particular loci;~~

hybridizing the at least one blocker ~~blockers~~ with the patient sample nucleic acid, ~~leaving~~ wherein at least one loci containing the genetic marker is unblocked;

providing ~~at least one~~ a detectable discriminator~~, the discriminator being~~ that is capable of binding with the at least one unblocked loci; and

hybridizing the ~~discriminators~~ discriminator with the at least one unblocked loci of the patient sample; [[and]]

detecting the ~~formation of a hyubridization event~~ genetic marker by detecting the presence of the discriminator.

2-4. (Cancelled)

5. (Currently Amended) [[A]] The method of claim 1, ~~for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 2,~~ wherein different blockers are provided to different sites.

6. (Currently Amended) The method ~~for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid~~ of claim 1, wherein the site comprises a site of an actively addressable electronic microarray.

7. (Currently Amended) The method ~~for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid~~ of claim 6, wherein the addressable electronic microarray includes a permeation layer.

8. (Currently Amended) The method ~~for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid~~ of claim 1, wherein the patient sample is amplified.

9. (Currently Amended) The ~~method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid~~ of claim 8, wherein the amplification includes polymerase chain reaction (PCR).

10. (Withdrawn) The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 8, wherein the amplification includes ligase chain reaction (LCR).

11. (Withdrawn) The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 8, wherein the amplification include strand displacement amplification (SDA).

12. (Withdrawn) The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 8, wherein the amplification includes the transcription-based amplification system (TAS).

13. (Withdrawn) The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 8, wherein the amplification includes the self-sustained sequence replication system (3SR).

14. (Withdrawn) The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 8, wherein the amplification includes the Qβ replicase amplification system (Qβ).

15-16. (Cancelled)

17. (Currently Amended) The method ~~for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid~~ of claim 1, wherein at least two loci are unblocked.

18. (Currently Amended) The method ~~for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid~~ of claim 1, further includes the step of performing a screening step.

19. (Currently Amended) The method ~~for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid~~ of claim 1, wherein the patient sample nucleic acid comprises multiple segments containing different loci.

20. (Currently Amended) The method ~~for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid~~ of claim 19, wherein the multiple segments containing different loci are affixed to the same site.

21. (Withdrawn) The method for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid of claim 19, wherein the multiple segments containing different loci are affixed to the different sites.

22. (Currently Amended) The method ~~for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid~~ of claim 6, wherein the multiple patient samples are provided on multiple sites of the microarray.

23. (Currently Amended) The method ~~for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid~~ of claim 1, further ~~including amplification controls indicated by different colors.~~ comprising the steps of:

providing a labeled amplification control that is capable of binding with the patient nucleic acid sample;

hybridizing the labeled amplification control to the patient nucleic acid sample.

24. (Currently Amended) The method ~~for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid~~ of claim 1, wherein the ~~loci are indicative of genetic diseases~~ genetic marker is indicative of a genetic disease.

25. (Currently Amended) The method ~~for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid~~ of claim 24, wherein the genetic disease is cystic fibrosis.

26. (Canceled)

27. (Currently Amended) The method ~~for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid~~ of claim 1, further ~~including a stabilizer adjacent the dsicriminator.~~ comprising the steps of:

providing a stabilizer that is capable of binding with the patient nucleic acid sample adjacent the at least one discriminator;

hybridizing the stabilizer to the patient nucleic acid sample.

28-44. (Cancelled)